

## **ABTS-07: Perth**

### **BREEDING OUTCOMES FROM MOLECULAR GENETICS**

*Jason Eglinton<sup>1</sup>, Stewart Coventry<sup>1</sup> and Ken Chalmers<sup>2</sup>*

<sup>1</sup>School of Agriculture, Food and Wine, Waite Campus, University of Adelaide.

<sup>2</sup>Molecular Plant Breeding CRC, Plant Genomics Centre, Waite Campus, University of Adelaide.

Molecular mapping, QTL analysis and marker assisted selection have been widely utilised in cereal breeding programs for the past 10 years, however there are few published examples of commercial varieties developed from these approaches. The current paper outlines successful examples from the University of Adelaide Barley Program, including outcomes from initial efforts in shifting allele frequencies in early generation populations and rapid backcrossing, through to whole genome based selection strategies.

Progress from more recent applications of molecular genetics to mainstream barley breeding will also be presented including;

- i. Advanced backcross (AB-QTL) populations for QTL identification and introgression
- ii. Genetic conversion of feed varieties to malting quality
- iii. Identification of the genomic regions responding to selection pressure applied during standard yield, agronomic and quality evaluation

**Theme:** Latest research & technology – breeding.

**Presentation type:** Oral Paper

**Presenter Profile:** Dr Eglinton completed a PhD studying the biochemistry and genetics of malting quality at the University of Adelaide, and then conducted an international research program developing barley for low rainfall environments in collaboration with ICARDA. Dr Eglinton was appointed as a barley breeder at the University of Adelaide in 2000, has been the Barley Program Leader since 2003. In addition to variety development, Dr Eglinton is responsible for a large scale research program addressing applied aspects of abiotic stress tolerance and malting quality.